SEQUENCE LISTING

<110> Schimmel, Paul
Wakasugi, Keisuke

<120> Human Aminoacyl-tRNA Synthetase Polypeptides Useful For The Regulation of Angiogenesis

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<170> PatentIn Ver. 2.0

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Thr Arg Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile
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ctg aag gag cgg gaa ctt aaa att tac tgg gga acg gca acc acg ggc   3565
Leu Lys Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly
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aaa cca cat gtg gct tac ttt gtg ccc atg tca aag att gca gac ttc   3613
Lys Pro His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe
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tta aag gca ggg tgt gag gta aca att ctg ttt gcg gac ctc cac gca   3661
Leu Lys Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala
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Tyr Leu Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Arg Val
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agt tac tat gag aat gtg atc aaa gca atg ctg gag agc att ggt gtg   3757
Ser Tyr Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val
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aaa gag tac aca cta gat gtg tac aga ctc tcc tcc gtg gtc aca cag   3853
Lys Glu Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln
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cac gat tcc aag aag gct gga gct gag gtg gta aag cag gtg gag cac   3901
His Asp Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His
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Glu Tyr Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys
175                 180                 185                 190

att ttc acc ttt gca gag aag tac ctc cct gca ctt ggc tat tca aaa   4045
Ile Phe Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys
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cgg gtc cat ctg atg aat cct atg gtt cca gga tta aca ggc agc aaa   4093
Arg Val His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys
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atg agc tct tca gaa gag gag tcc aag att gat ctc ctt gat cgg aag   4141
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gag gat gtg aag aaa aaa ctg aag aag gcc ttc tgt gag cca gga aat   4189
Glu Asp Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn
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gtg gag aac aat ggg gtt ctg tcc ttc atc aag cat gtc ctt ttt ccc   4237
Val Glu Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro
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ctt aag tcc gag ttt gtg atc cta cga gat gag aaa tgg ggt gga aac   4285
Leu Lys Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn
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aaa acc tac aca gct tac gtg gac ctg gaa aag gac ttt gct gct gag   4333
Lys Thr Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu
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gtt gta cat cct gga gac ctg aag aat tct gtt gaa gtc gca ctg aac   4381
Val Val His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn
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aag ttg ctg gat cca atc cgg gaa aag ttt aat acc cct gcc ctg aaa   4429
Lys Leu Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys
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aaa ctg gcc agc gct gcc tac cca gat ccc tca aag cag aag cca atg   4477
Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met
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gcc aaa ggc cct gcc aag aat tca gaa cca gag gag gtc atc cca tcc   4525
Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Pro Ser
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cgg ctg gat atc cgt gtg ggg aaa atc atc act gtg gag aag cac cca   4573
Arg Leu Asp Ile Arg Val Gly Lys Ile Ile Thr Val Glu Lys His Pro
            370                 375                 380

gat gca gac agc ctg tat gta gag aag att gac gtg ggg gaa gct gaa   4621
Asp Ala Asp Ser Leu Tyr Val Glu Lys Ile Asp Val Gly Glu Ala Glu
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cca cgg act gtg gtg agc ggc ctg gta cag ttc gtg ccc aag gag gaa   4669
Pro Arg Thr Val Val Ser Gly Leu Val Gln Phe Val Pro Lys Glu Glu
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ctg cag gac agg ctg gta gtg gtg ctg tgc aac ctg aaa ccc cag aag   4717
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atg aga gga gtc gag tcc caa ggc atg ctt ctg tgt gct tct ata gaa   4765
Met Arg Gly Val Glu Ser Gln Gly Met Leu Leu Cys Ala Ser Ile Glu
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ggg ata aac cgc cag gtt gaa cct ctg gac cct ccg gca ggc tct gct   4813
Gly Ile Asn Arg Gln Val Glu Pro Leu Asp Pro Pro Ala Gly Ser Ala
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cct ggt gag cac gtg ttt gtg aag ggc tat gaa aag ggc caa cca gat   4861
Pro Gly Glu His Val Phe Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp
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gag gag ctc aag ccc aag aag aaa gtc ttc gag aag ttg cag gct gac   4909
Glu Glu Leu Lys Pro Lys Lys Lys Val Phe Glu Lys Leu Gln Ala Asp
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ttc aaa att tct gag gag tgc atc gca cag tgg aag caa acc aac ttc   4957
Phe Lys Ile Ser Glu Glu Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe
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atg acc aag ctg ggc tcc att tcc tgt aaa tcg ctg aaa ggg ggg aac   5005
Met Thr Lys Leu Gly Ser Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn
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att agc ctc gag cac cac cac cac cac tgagatccgg ctgctaacaa        5055
Ile Ser Leu Glu His His His His His His
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His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe Leu Lys
     50                  55                  60
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Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Arg Val Ser Tyr
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Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val Pro Leu
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Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser Lys Glu
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Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln His Asp
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Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His Pro Leu
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Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu Glu Tyr
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Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys Ile Phe
180 185 190

Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys Arg Val
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His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys Met Ser
210 215 220

Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys Glu Asp
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Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn Val Glu
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Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro Leu Lys
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Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu Val Val
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His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn Lys Leu
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Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met Ala Lys
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Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Pro Ser Arg Leu
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Asp Ile Arg Val Gly Lys Ile Ile Thr Val Glu Lys His Pro Asp Ala
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Asp Ser Leu Tyr Val Glu Lys Ile Asp Val Gly Glu Ala Glu Pro Arg
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Thr Val Val Ser Gly Leu Val Gln Phe Val Pro Lys Glu Glu Leu Gln
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Asp Arg Leu Val Val Val Leu Cys Asn Leu Lys Pro Gln Lys Met Arg
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Gly Val Glu Ser Gln Gly Met Leu Leu Cys Ala Ser Ile Glu Gly Ile
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Glu His Val Phe Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp Glu Glu
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Leu Lys Pro Lys Lys Lys Val Phe Glu Lys Leu Gln Ala Asp Phe Lys
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Pro Leu Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser
                115                 120                 125

aaa gag tac aca cta gat gtg tac aga ctc tcc tcc gtg gtc aca cag   3853
Lys Glu Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln
            130                 135                 140

cac gat tcc aag aag gct gga gct gag gtg gta aag cag gtg gag cac   3901
His Asp Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His
        145                 150                 155

cct ttg ctg agt ggc ctc tta tac ccc gga ctg cag gct ttg gat gaa   3949
Pro Leu Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu
    160                 165                 170

gag tat tta aaa gta gat gcc caa ttt gga ggc att gat cag aga aag   3997
Glu Tyr Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys
175                 180                 185                 190

att ttc acc ttt gca gag aag tac ctc cct gca ctt ggc tat tca aaa   4045
Ile Phe Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys
                195                 200                 205

cgg gtc cat ctg atg aat cct atg gtt cca gga tta aca ggc agc aaa   4093
Arg Val His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys
            210                 215                 220

atg agc tct tca gaa gag gag tcc aag att gat ctc ctt gat cgg aag   4141
Met Ser Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys
        225                 230                 235

gag gat gtg aag aaa aaa ctg aag aag gcc ttc tgt gag cca gga aat   4189
Glu Asp Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn
    240                 245                 250

gtg gag aac aat ggg gtt ctg tcc ttc atc aag cat gtc ctt ttt ccc   4237
Val Glu Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro
255                 260                 265                 270

ctt aag tcc gag ttt gtg atc cta cga gat gag aaa tgg ggt gga aac   4285
Leu Lys Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn
                275                 280                 285

aaa acc tac aca gct tac gtg gac ctg gaa aag gac ttt gct gct gag   4333
Lys Thr Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu
            290                 295                 300

gtt gta cat cct gga gac ctg aag aat tct gtt gaa gtc gca ctg aac   4381
Val Val His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn
        305                 310                 315

aag ttg ctg gat cca atc cgg gaa aag ttt aat acc cct gcc ctg aaa   4429
Lys Leu Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys
    320                 325                 330

aaa ctg gcc agc gct gcc tac cca gat ccc tca aag cag aag cca atg   4477
Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met
335                 340                 345                 350
```

```
gcc aaa ggc cct gcc aag aat tca gaa cca gag gag gtc atc ctc gag   4525
Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu
                355                 360                 365

cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag          4573
His His His His His His
            370

gaagctgagt tggctgctgc caccgctgag caataactag cataacccct tggggcctct 4633

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat             4682
```

<210> 4
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human mini TyrRS in pET20B

<400> 4

```
Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile Thr Arg
  1               5                  10                  15

Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile Leu Lys
             20                  25                  30

Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly Lys Pro
         35                  40                  45

His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe Leu Lys
     50                  55                  60

Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala Tyr Leu
 65                  70                  75                  80

Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Arg Val Ser Tyr
                 85                  90                  95

Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val Pro Leu
            100                 105                 110

Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser Lys Glu
        115                 120                 125

Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln His Asp
    130                 135                 140

Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His Pro Leu
145                 150                 155                 160

Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu Glu Tyr
                165                 170                 175

Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys Ile Phe
            180                 185                 190

Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys Arg Val
        195                 200                 205
```

```
His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys Met Ser
    210                 215                 220

Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys Glu Asp
225                 230                 235                 240

Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn Val Glu
                245                 250                 255

Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro Leu Lys
            260                 265                 270

Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn Lys Thr
        275                 280                 285

Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu Val Val
    290                 295                 300

His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn Lys Leu
305                 310                 315                 320

Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys Lys Leu
                325                 330                 335

Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met Ala Lys
            340                 345                 350

Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu His His
        355                 360                 365

His His His His
    370
```

<210> 5
<211> 4100
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(3961)

<220>
<223> Description of Artificial Sequence: human TyrRS carboxyl-terminal domain in pET20B

<400> 5
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta taagggattt gccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg ctttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200

ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260

ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320

cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380

gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440

actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500

aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt ttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag gcgcagcggt cgggctgaac gggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220

cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt 2280

ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

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aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

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tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 3180

acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

tatacat atg cca gag gag gtc atc cca tcc cgg ctg gat atc cgt gtg 3469
Met Pro Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val
1 5 10

ggg aaa atc atc act gtg gag aag cac cca gat gca gac agc ctg tat 3517
Gly Lys Ile Ile Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr
15 20 25 30

gta gag aag att gac gtg ggg gaa gct gaa cca cgg act gtg gtg agc 3565
Val Glu Lys Ile Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser
35 40 45

ggc ctg gta cag ttc gtg ccc aag gag gaa ctg cag gac agg ctg gta 3613
Gly Leu Val Gln Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val
50 55 60

gtg gtg ctg tgc aac ctg aaa ccc cag aag atg aga gga gtc gag tcc 3661
Val Val Leu Cys Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser
65 70 75

caa ggc atg ctt ctg tgt gct tct ata gaa ggg ata aac cgc cag gtt 3709
Gln Gly Met Leu Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val
80 85 90

```
gaa cct ctg gac cct ccg gca ggc tct gct cct ggt gag cac gtg ttt   3757
Glu Pro Leu Asp Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe
 95                 100                 105                 110

gtg aag ggc tat gaa aag ggc caa cca gat gag gag ctc aag ccc aag   3805
Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys
                115                 120                 125

aag aaa gtc ttc gag aag ttg cag gct gac ttc aaa att tct gag gag   3853
Lys Lys Val Phe Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu
            130                 135                 140

tgc atc gca cag tgg aag caa acc aac ttc atg acc aag ctg ggc tcc   3901
Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser
        145                 150                 155

att tcc tgt aaa tcg ctg aaa ggg ggg aac att agc ctc gag cac cac   3949
Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn Ile Ser Leu Glu His His
    160                 165                 170

cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag gaagctgagt       4001
His His His His
175

tggctgctgc caccgctgag caataactag cataacccct tggggcctct aaacgggtct 4061

tgaggggttt tttgctgaaa ggaggaacta tatccggat                       4100
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<210> 6
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human TyrRS carboxyl-terminal domain in pET20B

<400> 6

```
Met Pro Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys
  1               5                  10                  15

Ile Ile Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu
             20                  25                  30

Lys Ile Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser Gly Leu
         35                  40                  45

Val Gln Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val Val Val
     50                  55                  60

Leu Cys Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser Gln Gly
 65                  70                  75                  80

Met Leu Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val Glu Pro
                 85                  90                  95

Leu Asp Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe Val Lys
            100                 105                 110

Gly Tyr Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys Lys Lys
        115                 120                 125
```

Val Phe Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu Cys Ile
130 135 140

Ala Gln Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser Ile Ser
145 150 155 160

Cys Lys Ser Leu Lys Gly Gly Asn Ile Ser Leu Glu His His His His
165 170 175

His His

<210> 7
<211> 4682
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(4543)

<220>
<223> Description of Artificial Sequence: human mini
TyrRS mutant in pET20B

<400> 7
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta taagggattt gccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg ctttttgca caacatgggg gatcatgtaa ctcgccttga 1080
tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140
tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200
ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260
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accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740
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cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160
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catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760
tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820
ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

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tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa 3000

aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 3180

acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

tatacat atg ggg gac gct ccc agc cct gaa gag aaa ctg cac ctt atc   3469
        Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile
          1               5                  10

acc cgg aac ctg cag gag gtt ctg ggg gaa gag aag ctg aag gag ata   3517
Thr Arg Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile
 15                  20                  25                  30

ctg aag gag cgg gaa ctt aaa att tac tgg gga acg gca acc acg ggc   3565
Leu Lys Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly
                 35                  40                  45

aaa cca cat gtg gct tac ttt gtg ccc atg tca aag att gca gac ttc   3613
Lys Pro His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe
             50                  55                  60

tta aag gca ggg tgt gag gta aca att ctg ttt gcg gac ctc cac gca   3661
Leu Lys Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala
         65                  70                  75

tac ctg gat aac atg aaa gcc cca tgg gaa ctt cta gaa ctg cag gtc   3709
Tyr Leu Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Gln Val
     80                  85                  90

agt tac tat gag aat gtg atc aaa gca atg ctg gag agc att ggt gtg   3757
Ser Tyr Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val
 95                  100                 105                 110

ccc ttg gag aag ctc aag ttc atc aaa ggc act gat tac cag ctc agc   3805
Pro Leu Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser
                115                 120                 125

aaa gag tac aca cta gat gtg tac aga ctc tcc tcc gtg gtc aca cag   3853
Lys Glu Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln
            130                 135                 140

cac gat tcc aag aag gct gga gct gag gtg gta aag cag gtg gag cac   3901
His Asp Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His
        145                 150                 155

cct ttg ctg agt ggc ctc tta tac ccc gga ctg cag gct ttg gat gaa   3949
Pro Leu Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu
    160                 165                 170
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gag tat tta aaa gta gat gcc caa ttt gga ggc att gat cag aga aag   3997
Glu Tyr Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys
175                 180                 185                 190

att ttc acc ttt gca gag aag tac ctc cct gca ctt ggc tat tca aaa   4045
Ile Phe Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys
                195                 200                 205

cgg gtc cat ctg atg aat cct atg gtt cca gga tta aca ggc agc aaa   4093
Arg Val His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys
            210                 215                 220

atg agc tct tca gaa gag gag tcc aag att gat ctc ctt gat cgg aag   4141
Met Ser Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys
        225                 230                 235

gag gat gtg aag aaa aaa ctg aag aag gcc ttc tgt gag cca gga aat   4189
Glu Asp Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn
    240                 245                 250

gtg gag aac aat ggg gtt ctg tcc ttc atc aag cat gtc ctt ttt ccc   4237
Val Glu Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro
255                 260                 265                 270

ctt aag tcc gag ttt gtg atc cta cga gat gag aaa tgg ggt gga aac   4285
Leu Lys Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn
                275                 280                 285

aaa acc tac aca gct tac gtg gac ctg gaa aag gac ttt gct gct gag   4333
Lys Thr Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu
            290                 295                 300

gtt gta cat cct gga gac ctg aag aat tct gtt gaa gtc gca ctg aac   4381
Val Val His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn
        305                 310                 315

aag ttg ctg gat cca atc cgg gaa aag ttt aat acc cct gcc ctg aaa   4429
Lys Leu Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys
    320                 325                 330

aaa ctg gcc agc gct gcc tac cca gat ccc tca aag cag aag cca atg   4477
Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met
335                 340                 345                 350

gcc aaa ggc cct gcc aag aat tca gaa cca gag gag gtc atc ctc gag   4525
Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu
                355                 360                 365

cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag          4573
His His His His His His
            370

gaagctgagt tggctgctgc caccgctgag caataactag cataaccccc tggggcctct 4633

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat             4682
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<210> 8
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human mini TyrRS mutant in pET20B

<400> 8

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Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile Thr Arg
 1               5                  10                  15

Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile Leu Lys
            20                  25                  30

Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly Lys Pro
        35                  40                  45

His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe Leu Lys
    50                  55                  60

Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala Tyr Leu
65                  70                  75                  80

Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Gln Val Ser Tyr
                85                  90                  95

Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val Pro Leu
            100                 105                 110

Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser Lys Glu
        115                 120                 125

Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln His Asp
    130                 135                 140

Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His Pro Leu
145                 150                 155                 160

Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu Glu Tyr
                165                 170                 175

Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys Ile Phe
            180                 185                 190

Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys Arg Val
        195                 200                 205

His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys Met Ser
    210                 215                 220

Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys Glu Asp
225                 230                 235                 240

Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn Val Glu
                245                 250                 255

Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro Leu Lys
            260                 265                 270
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Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn Lys Thr
275 280 285

Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu Val Val
290 295 300

His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn Lys Leu
305 310 315 320

Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys Lys Leu
325 330 335

Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met Ala Lys
340 345 350

Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu His His
355 360 365

His His His His
370

<210> 9
<211> 5018
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(4879)

<220>
<223> Description of Artificial Sequence: human
full-length TrpRS in pET20B

<400> 9
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg ctttttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

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ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260

ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320

cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380

gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440

actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500

aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt ttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag gcgcagcggt cgggctgaac gggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220

cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt 2280

ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

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gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa 3000

aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

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acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

tatacat atg ccc aac agt gag ccc gca tct ctg ctg gag ctg ttc aac   3469
        Met Pro Asn Ser Glu Pro Ala Ser Leu Leu Glu Leu Phe Asn
          1               5                  10

agc atc gcc aca caa ggg gag ctc gta agg tcc ctc aaa gcg gga aat   3517
Ser Ile Ala Thr Gln Gly Glu Leu Val Arg Ser Leu Lys Ala Gly Asn
 15                  20                  25                  30

gcg tca aag gat gaa att gat tct gca gta aag atg ttg gtg tca tta   3565
Ala Ser Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu
                 35                  40                  45

aaa atg agc tac aaa gct gcc gcg ggg gag gat tac aag gct gac tgt   3613
Lys Met Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys
             50                  55                  60

cct cca ggg aac cca gca cct acc agt aat cat ggc cca gat gcc aca   3661
Pro Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr
         65                  70                  75

gaa gct gaa gag gat ttt gtg gac cca tgg aca gta cag aca agc agt   3709
Glu Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser
     80                  85                  90

gca aaa ggc ata gac tac gat aag ctc att gtt cgg ttt gga agt agt   3757
Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser
 95                  100                 105                 110

aaa att gac aaa gag cta ata aac cga ata gag aga gcc acc ggc caa   3805
Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln
                115                 120                 125

aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc tca cac aga gat   3853
Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp
            130                 135                 140
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atg aat cag gtt ctt gat gcc tat gaa aat aag aag cca ttt tat ctg    3901
Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu
        145                 150                 155

tac acg ggc cgg ggc ccc tct tct gaa gca atg cat gta ggt cac ctc    3949
Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu
    160                 165                 170

att cca ttt att ttc aca aag tgg ctc cag gat gta ttt aac gtg ccc    3997
Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro
175                 180                 185                 190

ttg gtc atc cag atg acg gat gac gag aag tat ctg tgg aag gac ctg    4045
Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu
                195                 200                 205

acc ctg gac cag gcc tat ggc gat gct gtt gag aat gcc aag gac atc    4093
Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile
            210                 215                 220

atc gcc tgt ggc ttt gac atc aac aag act ttc ata ttc tct gac ctg    4141
Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu
        225                 230                 235

gac tac atg ggg atg agc tca ggt ttc tac aaa aat gtg gtg aag att    4189
Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile
    240                 245                 250

caa aag cat gtt acc ttc aac caa gtg aaa ggc att ttc ggc ttc act    4237
Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr
255                 260                 265                 270

gac agc gac tgc att ggg aag atc agt ttt cct gcc atc cag gct gct    4285
Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala
                275                 280                 285

ccc tcc ttc agc aac tca ttc cca cag atc ttc cga gac agg acg gat    4333
Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp
            290                 295                 300

atc cag tgc ctt atc cca tgt gcc att gac cag gat cct tac ttt aga    4381
Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg
        305                 310                 315

atg aca agg gac gtc gcc ccc agg atc ggc tat cct aaa cca gcc ctg    4429
Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu
    320                 325                 330

ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc cag acc aaa atg    4477
Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met
335                 340                 345                 350

agt gcc agc gac cca aac tcc tcc atc ttc ctc acc gac acg gcc aag    4525
Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys
                355                 360                 365

cag atc aaa acc aag gtc aat aag cat gcg ttt tct gga ggg aga gac    4573
Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp
            370                 375                 380
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```
acc atc gag gag cac agg cag ttt ggg ggc aac tgt gat gtg gac gtg   4621
Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val
        385                 390                 395

tct ttc atg tac ctg acc ttc ttc ctc gag gac gac gac aag ctc gag   4669
Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu
    400                 405                 410

cag atc agg aag gat tac acc agc gga gcc atg ctc acc ggt gag ctc   4717
Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu
415                 420                 425                 430

aag aag gca ctc ata gag gtt ctg cag ccc ttg atc gca gag cac cag   4765
Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln
                435                 440                 445

gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa gag ttc atg act   4813
Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr
            450                 455                 460

ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg gcc gca ctc gag   4861
Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu
        465                 470                 475

cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag          4909
His His His His His His
    480

gaagctgagt tggctgctgc caccgctgag caataactag cataacccct tggggcctct 4969

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat             5018
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<210> 10
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human full-length TrpRS in pET20B

<400> 10

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Met Pro Asn Ser Glu Pro Ala Ser Leu Leu Glu Leu Phe Asn Ser Ile
  1               5                  10                  15

Ala Thr Gln Gly Glu Leu Val Arg Ser Leu Lys Ala Gly Asn Ala Ser
             20                  25                  30

Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu Lys Met
         35                  40                  45

Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro
     50                  55                  60

Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala
 65                  70                  75                  80

Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys
                 85                  90                  95
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Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile
100 105 110

Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro
115 120 125

His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn
130 135 140

Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr
145 150 155 160

Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro
165 170 175

Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val
180 185 190

Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu
195 200 205

Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala
210 215 220

Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr
225 230 235 240

Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys
245 250 255

His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser
260 265 270

Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser
275 280 285

Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln
290 295 300

Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr
305 310 315 320

Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His
325 330 335

Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala
340 345 350

Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile
355 360 365

Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile
370 375 380

Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe
385 390 395 400

Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile
405 410 415

Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys
420 425 430

```
Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg
        435                 440                 445

Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg
    450                 455                 460

Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His His
465                 470                 475                 480

His His His His
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<210> 11
<211> 4877
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(4738)

<220>
<223> Description of Artificial Sequence: human mini TrpRS in pET20B

<400> 11
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ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta taagggattt gccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg ctttttgca caacatgggg gatcatgtaa ctcgccttga 1080

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aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag gcgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220

cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt 2280

ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

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tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa 3000

aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 3180

acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

tatacat atg agc tac aaa gct gcc gcg ggg gag gat tac aag gct gac    3469
        Met Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp
         1               5                  10

tgt cct cca ggg aac cca gca cct acc agt aat cat ggc cca gat gcc    3517
Cys Pro Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala
 15                  20                  25                  30

aca gaa gct gaa gag gat ttt gtg gac cca tgg aca gta cag aca agc    3565
Thr Glu Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser
                 35                  40                  45

agt gca aaa ggc ata gac tac gat aag ctc att gtt cgg ttt gga agt    3613
Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser
             50                  55                  60

agt aaa att gac aaa gag cta ata aac cga ata gag aga gcc acc ggc    3661
Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly
         65                  70                  75

caa aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc tca cac aga    3709
Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg
     80                  85                  90

gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag cca ttt tat    3757
Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr
 95                 100                 105                 110

ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat gta ggt cac    3805
Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His
                115                 120                 125

ctc att cca ttt att ttc aca aag tgg ctc cag gat gta ttt aac gtg    3853
Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val
            130                 135                 140

ccc ttg gtc atc cag atg acg gat gac gag aag tat ctg tgg aag gac    3901
Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp
        145                 150                 155

ctg acc ctg gac cag gcc tat ggc gat gct gtt gag aat gcc aag gac    3949
Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp
    160                 165                 170
```

atc atc gcc tgt ggc ttt gac atc aac aag act ttc ata ttc tct gac 3997
Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp
175 180 185 190

ctg gac tac atg ggg atg agc tca ggt ttc tac aaa aat gtg gtg aag 4045
Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys
195 200 205

att caa aag cat gtt acc ttc aac caa gtg aaa ggc att ttc ggc ttc 4093
Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe
210 215 220

act gac agc gac tgc att ggg aag atc agt ttt cct gcc atc cag gct 4141
Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala
225 230 235

gct ccc tcc ttc agc aac tca ttc cca cag atc ttc cga gac agg acg 4189
Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr
240 245 250

gat atc cag tgc ctt atc cca tgt gcc att gac cag gat cct tac ttt 4237
Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe
255 260 265 270

aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct aaa cca gcc 4285
Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala
275 280 285

ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc cag acc aaa 4333
Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys
290 295 300

atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc gac acg gcc 4381
Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala
305 310 315

aag cag atc aaa acc aag gtc aat aag cat gcg ttt tct gga ggg aga 4429
Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg
320 325 330

gac acc atc gag gag cac agg cag ttt ggg ggc aac tgt gat gtg gac 4477
Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp
335 340 345 350

gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac gac aag ctc 4525
Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu
355 360 365

gag cag atc agg aag gat tac acc agc gga gcc atg ctc acc ggt gag 4573
Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu
370 375 380

ctc aag aag gca ctc ata gag gtt ctg cag ccc ttg atc gca gag cac 4621
Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His
385 390 395

cag gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa gag ttc atg 4669
Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met
400 405 410

```
act ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg gcc gca ctc   4717
Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu
415                 420                 425                 430

gag cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag      4768
Glu His His His His His His
                435

gaagctgagt tggctgctgc caccgctgag caataactag cataacccct tggggcctct 4828

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat             4877
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<210> 12
<211> 437
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human mini TrpRS in pET20B

<400> 12

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Met Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro
  1               5                  10                  15

Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu
             20                  25                  30

Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala
         35                  40                  45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys
     50                  55                  60

Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
 65                  70                  75                  80

Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met
                 85                  90                  95

Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr
            100                 105                 110

Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile
        115                 120                 125

Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu
    130                 135                 140

Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr
145                 150                 155                 160

Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile
                165                 170                 175

Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp
            180                 185                 190

Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln
        195                 200                 205
```

Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp
210 215 220

Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro
225 230 235 240

Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile
245 250 255

Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met
260 265 270

Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu
275 280 285

His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser
290 295 300

Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln
305 310 315 320

Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr
325 330 335

Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser
340 345 350

Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln
355 360 365

Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys
370 375 380

Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala
385 390 395 400

Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro
405 410 415

Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His
420 425 430

His His His His His
435

<210> 13
<211> 4811
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(4672)

<220>
<223> Description of Artificial Sequence: human supermini TrpRS in pET20B

<400> 13
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cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg ctttttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

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ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260

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cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380

gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440

actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500

aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

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accggataag gcgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220

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ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

tttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

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acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

tatacat atg agt aat cat ggc cca gat gcc aca gaa gct gaa gag gat    3469
        Met Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp
         1               5                  10

ttt gtg gac cca tgg aca gta cag aca agc agt gca aaa ggc ata gac    3517
Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp
 15                  20                  25                  30

tac gat aag ctc att gtt cgg ttt gga agt agt aaa att gac aaa gag    3565
Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu
                35                  40                  45
```

```
cta ata aac cga ata gag aga gcc acc ggc caa aga cca cac cac ttc   3613
Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe
            50                  55                  60

ctg cgc aga ggc atc ttc ttc tca cac aga gat atg aat cag gtt ctt   3661
Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu
        65                  70                  75

gat gcc tat gaa aat aag aag cca ttt tat ctg tac acg ggc cgg ggc   3709
Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly
    80                  85                  90

ccc tct tct gaa gca atg cat gta ggt cac ctc att cca ttt att ttc   3757
Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe
95                  100                 105                 110

aca aag tgg ctc cag gat gta ttt aac gtg ccc ttg gtc atc cag atg   3805
Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met
                115                 120                 125

acg gat gac gag aag tat ctg tgg aag gac ctg acc ctg gac cag gcc   3853
Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala
            130                 135                 140

tat ggc gat gct gtt gag aat gcc aag gac atc atc gcc tgt ggc ttt   3901
Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe
        145                 150                 155

gac atc aac aag act ttc ata ttc tct gac ctg gac tac atg ggg atg   3949
Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met
    160                 165                 170

agc tca ggt ttc tac aaa aat gtg gtg aag att caa aag cat gtt acc   3997
Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr
175                 180                 185                 190

ttc aac caa gtg aaa ggc att ttc ggc ttc act gac agc gac tgc att   4045
Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile
                195                 200                 205

ggg aag atc agt ttt cct gcc atc cag gct gct ccc tcc ttc agc aac   4093
Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn
            210                 215                 220

tca ttc cca cag atc ttc cga gac agg acg gat atc cag tgc ctt atc   4141
Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile
        225                 230                 235

cca tgt gcc att gac cag gat cct tac ttt aga atg aca agg gac gtc   4189
Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val
    240                 245                 250

gcc ccc agg atc ggc tat cct aaa cca gcc ctg ttg cac tcc acc ttc   4237
Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe
255                 260                 265                 270

ttc cca gcc ctg cag ggc gcc cag acc aaa atg agt gcc agc gac cca   4285
Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro
                275                 280                 285
```

```
aac tcc tcc atc ttc ctc acc gac acg gcc aag cag atc aaa acc aag   4333
Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys
            290                 295                 300

gtc aat aag cat gcg ttt tct gga ggg aga gac acc atc gag gag cac   4381
Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His
        305                 310                 315

agg cag ttt ggg ggc aac tgt gat gtg gac gtg tct ttc atg tac ctg   4429
Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu
    320                 325                 330

acc ttc ttc ctc gag gac gac gac aag ctc gag cag atc agg aag gat   4477
Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp
335                 340                 345                 350

tac acc agc gga gcc atg ctc acc ggt gag ctc aag aag gca ctc ata   4525
Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile
                355                 360                 365

gag gtt ctg cag ccc ttg atc gca gag cac cag gcc cgg cgc aag gag   4573
Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu
            370                 375                 380

gtc acg gat gag ata gtg aaa gag ttc atg act ccc cgg aag ctg tcc   4621
Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser
        385                 390                 395

ttc gac ttt cag aag ctt gcg gcc gca ctc gag cac cac cac cac cac   4669
Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His His His His His
    400                 405                 410

cac tgagatccgg ctgctaacaa agcccgaaag gaagctgagt tggctgctgc        4722
His
415

caccgctgag caataactag cataacccct tggggcctct aaacgggtct tgaggggttt 4782

tttgctgaaa ggaggaacta tatccggat                                   4811
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<210> 14
<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human supermini TrpRS in pET20B

<400> 14

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Met Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp Phe Val
  1               5                  10                  15

Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp Tyr Asp
             20                  25                  30

Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu Leu Ile
         35                  40                  45

Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe Leu Arg
     50                  55                  60
```

```
Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu Asp Ala
65                  70                  75                  80

Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser
                85                  90                  95

Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys
            100                 105                 110

Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp
        115                 120                 125

Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly
    130                 135                 140

Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile
145                 150                 155                 160

Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser
                165                 170                 175

Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr Phe Asn
            180                 185                 190

Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys
        195                 200                 205

Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe
    210                 215                 220

Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys
225                 230                 235                 240

Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro
                245                 250                 255

Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro
            260                 265                 270

Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser
        275                 280                 285

Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn
    290                 295                 300

Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln
305                 310                 315                 320

Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe
                325                 330                 335

Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr
            340                 345                 350

Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val
        355                 360                 365

Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr
    370                 375                 380
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Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp
385 390 395 400

Phe Gln Lys Leu Ala Ala Ala Leu Glu His His His His His His
405 410 415

<210> 15
<211> 4742
<212> DNA
<213> Artificial Sequence

<220>
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<222> (3428)..(4603)

<220>
<223> Description of Artificial Sequence: human minor Trp-RS fragment in pET20B

<400> 15
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60

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ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta taagggattt gccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg ctttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200

ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260

ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320

cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380

gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440

actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500

aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag gcgcagcggt cgggctgaac gggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220

cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt 2280

ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

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gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa 3000

aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

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gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 3180

acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

tatacat atg agt gca aaa ggc ata gac tac gat aag ctc att gtt cgg   3469
        Met Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg
          1               5                  10

ttt gga agt agt aaa att gac aaa gag cta ata aac cga ata gag aga   3517
Phe Gly Ser Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg
 15                  20                  25                  30

gcc acc ggc caa aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc   3565
Ala Thr Gly Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe
                 35                  40                  45

tca cac aga gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag   3613
Ser His Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys
             50                  55                  60

cca ttt tat ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat   3661
Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His
         65                  70                  75

gta ggt cac ctc att cca ttt att ttc aca aag tgg ctc cag gat gta   3709
Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val
     80                  85                  90

ttt aac gtg ccc ttg gtc atc cag atg acg gat gac gag aag tat ctg   3757
Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu
 95                  100                 105                 110

tgg aag gac ctg acc ctg gac cag gcc tat ggc gat gct gtt gag aat   3805
Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn
                115                 120                 125

gcc aag gac atc atc gcc tgt ggc ttt gac atc aac aag act ttc ata   3853
Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile
            130                 135                 140

ttc tct gac ctg gac tac atg ggg atg agc tca ggt ttc tac aaa aat   3901
Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn
        145                 150                 155

gtg gtg aag att caa aag cat gtt acc ttc aac caa gtg aaa ggc att   3949
Val Val Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile
    160                 165                 170

ttc ggc ttc act gac agc gac tgc att ggg aag atc agt ttt cct gcc   3997
Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala
175                 180                 185                 190
```

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atc cag gct gct ccc tcc ttc agc aac tca ttc cca cag atc ttc cga   4045
Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg
                195                 200                 205

gac agg acg gat atc cag tgc ctt atc cca tgt gcc att gac cag gat   4093
Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp
            210                 215                 220

cct tac ttt aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct   4141
Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro
        225                 230                 235

aaa cca gcc ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc   4189
Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala
    240                 245                 250

cag acc aaa atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc   4237
Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr
255                 260                 265                 270

gac acg gcc aag cag atc aaa acc aag gtc aat aag cat gcg ttt tct   4285
Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser
                275                 280                 285

gga ggg aga gac acc atc gag gag cac agg cag ttt ggg ggc aac tgt   4333
Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys
            290                 295                 300

gat gtg gac gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac   4381
Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp
        305                 310                 315

gac aag ctc gag cag atc agg aag gat tac acc agc gga gcc atg ctc   4429
Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu
    320                 325                 330

acc ggt gag ctc aag aag gca ctc ata gag gtt ctg cag ccc ttg atc   4477
Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile
335                 340                 345                 350

gca gag cac cag gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa   4525
Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys
                355                 360                 365

gag ttc atg act ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg   4573
Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala
            370                 375                 380

gcc gca ctc gag cac cac cac cac cac cac tgagatccgg ctgctaacaa     4623
Ala Ala Leu Glu His His His His His His
        385                 390

agcccgaaag gaagctgagt tggctgctgc caccgctgag caataactag cataacccct 4683

tggggcctct aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat  4742
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<210> 16
<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human minor TrpRS fragment in pET20B

<400> 16

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Met Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly
  1               5                  10                  15

Ser Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr
             20                  25                  30

Gly Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His
         35                  40                  45

Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe
     50                  55                  60

Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly
 65                  70                  75                  80

His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn
                 85                  90                  95

Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys
            100                 105                 110

Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys
        115                 120                 125

Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser
    130                 135                 140

Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val
145                 150                 155                 160

Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly
                165                 170                 175

Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln
            180                 185                 190

Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg
        195                 200                 205

Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr
    210                 215                 220

Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro
225                 230                 235                 240

Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr
                245                 250                 255

Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr
            260                 265                 270
```

```
Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly
        275                 280                 285

Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val
    290                 295                 300

Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys
305                 310                 315                 320

Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly
                325                 330                 335

Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu
            340                 345                 350

His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe
        355                 360                 365

Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala
    370                 375                 380

Leu Glu His His His His His His
385                 390


<210> 17
<211> 6
<212> PRT
<213> Homo sapiens

<400> 17
Glu Leu Arg Val Ser Tyr
  1               5


<210> 18
<211> 6
<212> PRT
<213> Escherichia coli

<400> 18
Glu Thr Val Gln Glu Trp
  1               5


<210> 19
<211> 9
<212> PRT
<213> Homo sapiens

<400> 19
Ser Ala Lys Glu Leu Arg Cys Gln Cys
  1               5
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<210> 20
<211> 11
<212> PRT
<213> Homo sapiens

<400> 20
Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys
1 5 10

<210> 21
<211> 7
<212> PRT
<213> Homo sapiens

<400> 21
Ala Glu Leu Arg Cys Gln Cys
1 5

<210> 22
<211> 58
<212> PRT
<213> Homo sapiens

<400> 22
Gly Asp Glu Lys Lys Ala Lys Glu Lys Ile Glu Lys Lys Gly Glu Lys
1 5 10 15

Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser Ala Asp Ser Lys Pro
20 25 30

Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly Cys Ile Ile Thr Ala
35 40 45

Arg Lys His Pro Asp Ala Asp Ser Leu Tyr
50 55

<210> 23
<211> 58
<212> PRT
<213> Homo sapiens

<400> 23
Pro Ala Leu Lys Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys
1 5 10 15

Gln Lys Pro Met Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu
20 25 30

Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys Ile Ile Thr Val
35 40 45

Glu Lys His Pro Asp Ala Asp Ser Leu Tyr
50 55

<210> 24
<211> 7
<212> PRT
<213> Homo sapiens

<400> 24
Arg Val Gly Lys Ile Ile Thr
1 5

<210> 25
<211> 7
<212> PRT
<213> Homo sapiens

<400> 25
Arg Ile Gly Cys Ile Ile Thr
1 5

<210> 26
<211> 7
<212> PRT
<213> Homo sapiens

<400> 26
Arg Ile Gly Arg Ile Ile Thr
1 5

<210> 27
<211> 7
<212> PRT
<213> Caenorhabditis elegans

<400> 27
Arg Val Gly Arg Ile Ile Lys
1 5

<210> 28
<211> 7
<212> PRT
<213> Saccharomyces cerevisiae

<400> 28
Arg Val Gly Phe Ile Gln Lys
1 5

<210> 29
<211> 7
<212> PRT
<213> Bos taurus

<400> 29
Arg Val Gly Lys Val Ile Ser
1 5

<210> 30
<211> 7
<212> PRT
<213> Mus musculus

<400> 30

Arg Ile Gly Cys Ile Val Thr
1 5

<210> 31
<211> 7
<212> PRT
<213> Mesocricetus auratus

<400> 31
Arg Ile Gly Arg Ile Val Thr
1 5

<210> 32
<211> 7
<212> PRT
<213> Ovis aries

<400> 32
Arg Ile Gly Cys Ile Ile Thr
1 5

<210> 33
<211> 7
<212> PRT
<213> Calcarea sp.

<400> 33
Arg Ile Gly Arg Ile Thr Ser
1 5

<210> 34
<211> 7
<212> PRT
<213> A. aeolicus

<400> 34
Arg Val Ala Lys Val Leu Ser
1 5

<210> 35
<211> 7
<212> PRT
<213> Escherichia coli

<400> 35
Arg Val Gly Lys Ile Val Glu
1 5

<210> 36
<211> 7
<212> PRT
<213> Escherichia coli

<400> 36
Arg Val Ala Leu Ile Glu Asn
1 5

<210> 37
<211> 7
<212> PRT
<213> Haemophilus influenzae

<400> 37
Arg Val Ala Lys Val Leu Lys
1 5

<210> 38
<211> 7
<212> PRT
<213> Bacillus subtilis

<400> 38
Arg Val Ala Glu Val Ile Glu
1 5

<210> 39
<211> 7
<212> PRT
<213> B. stearothermophilus

<400> 39
Arg Val Ala Glu Val Val Gln
1 5

<210> 40
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 40
Arg Val Ala Glu Val Leu Ala
1 5

<210> 41
<211> 6
<212> PRT
<213> Escherichia coli

<400> 41
Val Gly Glu Val Val Glu
1 5

<210> 42
<211> 6
<212> PRT
<213> Bacillus subtilis

<400> 42
Ile Gly His Val Leu Glu
1 5

<210> 43
<211> 6
<212> PRT
<213> Synechococcus sp.

<400> 43
Val Gly Arg Val Leu Glu
1 5

<210> 44
<211> 6
<212> PRT
<213> Thermus thermophilus

<400> 44
Phe Ala Arg Val Leu Glu
1 5

<210> 45
<211> 85
<212> PRT
<213> Homo sapiens

<400> 45
Met Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro
1 5 10 15

Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu
20 25 30

Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala
35 40 45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys
50 55 60

Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
65 70 75 80

Pro His His Phe Leu
85

<210> 46
<211> 85
<212> PRT
<213> Bos taurus

<400> 46
Thr Ser Tyr Lys Ala Ala Thr Gly Glu Asp Tyr Lys Val Asp Cys Pro
1 5 10 15

Pro Gly Asp Pro Ala Pro Glu Ser Gly Glu Gly Leu Asp Ala Thr Glu
20 25 30

Ala Asp Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala
35 40 45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys
50 55 60

Ile Asp Lys Glu Leu Val Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
65 70 75 80

Pro His Arg Phe Leu
85

<210> 47
<211> 85
<212> PRT
<213> Mus musculus

<400> 47
Met Ser Tyr Lys Ala Ala Met Gly Glu Glu Tyr Lys Ala Gly Cys Pro
1 5 10 15

Pro Gly Asn Pro Thr Ala Gly Arg Asn Cys Asp Ser Asp Ala Thr Lys
20 25 30

Ala Ser Glu Asp Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala
35 40 45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Gln Pro Gly Ser Ser Lys
50 55 60

Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
65 70 75 80

Pro His Arg Phe Leu
85

<210> 48
<211> 85
<212> PRT
<213> Oryctolagus cuniculus

<400> 48
Thr Ser Tyr Lys Glu Ala Met Gly Glu Asp Tyr Lys Ala Asp Cys Pro
1 5 10 15

Pro Gly Asn Ser Thr Pro Asp Ser His Gly Pro Asp Glu Ala Val Asp
20 25 30

Asp Lys Glu Asp Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala
35 40 45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Gln Phe Gly Ser Ser Lys
50 55 60

Ile Asp Lys Glu Leu Val Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
65 70 75 80

Pro His Arg Phe Leu
85

<210> 49
<211> 86
<212> PRT
<213> Homo sapiens

<400> 49
Ile Ser Tyr Gln Gly Arg Ile Pro Tyr Pro Arg Pro Gly Thr Cys Pro
1 5 10 15

Gly Gly Ala Phe Thr Pro Asn Met Arg Thr Thr Lys Glu Phe Pro Asp
20 25 30

Asp Val Val Thr Phe Ile Arg Asn His Pro Leu Met Tyr Asn Ser Ile
35 40 45

Tyr Pro Ile His Lys Arg Pro Leu Ile Val Arg Ile Gly Thr Asp Tyr
50 55 60

Lys Tyr Thr Lys Ile Ala Val Asp Arg Val Asn Ala Ala Asp Gly Arg
65 70 75 80

Tyr His Val Leu Phe Leu
85

<210> 50
<211> 86
<212> PRT
<213> Mus musculus

<400> 50
Ile Ser Tyr Gln Gly Arg Ile Pro Tyr Pro Arg Pro Gly Thr Cys Pro
1 5 10 15

Gly Gly Ala Phe Thr Pro Asn Met Arg Thr Thr Lys Asp Phe Pro Asp
20 25 30

Asp Val Val Thr Phe Ile Arg Asn His Pro Leu Met Tyr Asn Ser Ile
35 40 45

Ser Pro Ile His Arg Arg Pro Leu Ile Val Arg Ile Gly Thr Asp Tyr
50 55 60

Lys Tyr Thr Lys Ile Ala Val Asp Arg Val Asn Ala Ala Asp Gly Arg
65 70 75 80

Tyr His Val Leu Phe Leu
85

<210> 51
<211> 46
<212> PRT
<213> Homo sapiens

<400> 51
Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro Gly Asn Pro
1 5 10 15

Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp
20 25 30

```
Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly
        35                  40                  45
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<210> 52
<211> 46
<212> PRT
<213> Bos taurus

<400> 52
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Ala Ala Thr Gly Glu Asp Tyr Lys Val Asp Cys Pro Pro Gly Asp Pro
  1               5                  10                  15

Ala Pro Glu Ser Gly Glu Gly Leu Asp Ala Thr Glu Ala Asp Glu Asp
             20                  25                  30

Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly
        35                  40                  45
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<210> 53
<211> 46
<212> PRT
<213> Mus musculus

<400> 53
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Ala Ala Met Gly Glu Glu Tyr Lys Ala Gly Cys Pro Pro Gly Asn Pro
  1               5                  10                  15

Thr Ala Gly Arg Asn Cys Asp Ser Asp Ala Thr Lys Ala Ser Glu Asp
             20                  25                  30

Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala Lys Gly
        35                  40                  45
```

<210> 54
<211> 46
<212> PRT
<213> Oryctolagus cuniculus

<400> 54
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Glu Ala Met Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro Gly Asn Ser
  1               5                  10                  15

Thr Pro Asp Ser His Gly Pro Asp Glu Ala Val Asp Asp Lys Glu Asp
             20                  25                  30

Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala Lys Gly
        35                  40                  45
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<210> 55
<211> 41
<212> PRT
<213> Mus musculus

<400> 55
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Ala Phe Ala Gly Glu Asp Phe Lys Val Asp Ile Pro Glu Thr His Gly
  1               5                  10                  15
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Gly Glu Gly Thr Glu Asp Glu Ile Asp Asp Glu Tyr Glu Gly Asp Trp
20 25 30

Ser Asn Ser Ser Ser Ser Thr Ser Gly
35 40

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